

PEM's
complete with table # 25 (PEM3) + # 47 (PEM6) are G1, rest are G3

Table 1. Previously characterized and novel Pan Endothelial Markers. The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 86,894 and 86,688 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUVEC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUVEC SAGE library contained 290,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8x10⁶ tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Velculescu et al. (Nat Genet 1999 Dec23(4):387-9).

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	CATATCATTA	247	501	130	87	2	angiomodulin (ANG), IGFBP-7, IGFBP-rP1, Mac25, TAF
2	TGCACTTCAAG	328	141	0	0	0	hevin
3	TTTGACCTTT	165	84	191	115	4	connective tissue growth factor (CTGF, IGFBP-rP2)
4	CCCTTGTCGG	131	104	1	1	0	EST's
5	TTGCTGACTTT	73	131	2	14	1	collagen, type VI, alpha 1
6	ACCATTTGGATT	102	67	0	0	2	Interferon induced transmembrane protein 1 (9-27, Leu 13)
7	ACACTTCTTTC	104	44	60	62	2	guanine nucleotide binding protein 11
8	TTCTGTCTTGT	71	67	118	72	0	von Willebrand factor
9	TCCTCTGCAGA	66	68	3	13	3	cysteine-rich protein 2 (CRP-2, ESP-1, SmLIM)
10	TATCTCTCAAG	26	106	34	16	1	collagen, type XVIII, alpha 1
11	ATGCTTTTGT	58	65	17	17	3	Insulin-like growth factor-binding protein 4
12	GGGATTAAAGC	40	67	30	14	2	CD148 (S-Endo 1, P1H12, Muc18, MCAM, Mel-CAM)
13	TTAGTTCGTA	38	69	9	13	0	SPARC (osteonectin, BM-40)
14	TTCTCCCAAT	20	86	16	64	2	collagen, type IV, alpha 2
15	GTGCTAAGCGG	24	74	0	10	2	collagen, type VI, alpha 2
16	GTTTATGGATA	35	58	11	11	1	matrix G1e protein (MGP)
17	CCCTTTCACAC	52	33	0	0	0	EST's, Weakly similar to HPER17 protein
18	TGTTCTGGAGA	58	27	18	56	2	gap junction protein, alpha 1, 43KD (connexin 43)
19	AAGATCAAGAT	34	50	2	4	1	actin, alpha 1, skeletal muscle with thrombospondin type 1 motif, 4)
20	TCTCTGAGCAT	32	48	0	0	0	aggrucanase 1 (metallicproteinase with thrombospondin type 1 motif, 4)
21	CAGGTTTCATA	22	56	0	0	0	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAF)
22	GCACAAGTTCT	43	25	6	22	0	calicronin receptor-like receptor activity modifying protein 2
23	AGCTTGTGGCC	45	23	0	0	0	calicronin receptor-like receptor activity modifying protein 3
24	CTTCTGGATAA	13	54	12	0	0	cell division cycle 42 (GTP-binding protein, 25KD)
25	CAACAATAA	42	25	13	6	0	EST's

26	ACCGGGCCGG	50	15	0	0	0	0	tetranectin (plasminogen-binding protein)
27	GGAAGCTAAGT	35	27	0	5	1	0	osteoblast specific factor 2 (fasciilin-like)
28	GGAATTTAACC	38	21	0	3	0	0	solute carrier family 21 (prostaglandin transporter), member 2
29	GATAACTACAT	18	35	4	4	0	0	angiomodulin (ANG, IGFBP-7, IGFBP-P1, Mac25, TAF)
30	TATGAGGGTAA	19	30	40	2	0	0	regulator of G-protein signalling 5
31	CCAGGGGATTC	10	39	0	0	0	0	collagen, type III, alpha 1
32	TTTACCAAGAG	22	21	0	1	1	0	carboxypeptidase E
33	CCCAGTAAGAT	26	25	0	16	1	0	cysteine and glycine-rich factor 2 (LIM domain only, smooth muscle)
34	ACAAAGCATTT	26	20	0	14	1	0	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA
35	CGCTGTCCCTG	8	38	22	11	0	0	ESTs / biglycan
36	TACTTTAATG	25	21	1	1	0	0	metalloproteinase with thrombospondin type 1 motifs (ADAMTS1, METH-1)
37	TGTTTAATACA	15	29	2	1	1	0	ESTs / sry/hocoyte membrane protein band 4.1-like 2
38	GTCCCTGCCTT	18	25	1	1	0	0	glutathione S-transferase M2 (muscle)
39	GAGGCATCAT	21	21	2	2	1	0	ESTs / GTP-binding protein overexpressed in skeletal muscle
40	GCCCTACAGT	26	13	2	3	0	0	ESTs / KIA0821 protein
41	GCTACCCCTG	7	31	0	1	0	0	ESTs
42	ATCACACAGCT	19	18	0	0	0	0	thyroid and eye muscle autoantigen D1 (84kD)
43	ACAAGTACTGT	18	19	36	27	0	0	cadherin 5, VE-cadherin (vascular epithelium)
44	TCACGGCTGGAC	20	17	0	1	0	0	selectin P (granule membrane protein 140kD, antigen CD82)
45	ACATTCCAAGT	18	18	0	1	1	0	tissue inhibitor of metalloproteinase 3
46	GAGCCTGGAA	6	29	0	0	0	0	chondroitin sulfate proteoglycan 4 (melanoma-associated)
47	GGCACTCCTGT	22	13	19	12	0	0	ESTs
48	TCACAGCCCC	20	15	8	5	0	0	albumin
49	TGCCAGGTGCA	10	23	0	1	0	0	ESTs
50	TGGAAACCTG	11	22	0	1	1	0	eukaryotic translation initiation factor 4 gamma, 1
51	TTTATCATCCT	20	13	0	2	0	0	ESTs, KIA0382 protein
52	ACAGGGGGCA	15	18	0	0	1	0	Interferon, alpha-inducible protein (clone IFI-6-16)
53	ACTGAAGAAG	6	26	0	0	1	0	complement component 1, s subcomponent
54	ACCGTTCTGTA	8	24	10	6	0	0	transcription factor 4
55	ATACATAATT	25	6	12	0	0	0	ESTs
56	TTTGATATAGAA	17	15	4	5	1	0	hect domain and RLD 2
57	GTAATGACAGA	20	11	1	1	1	0	slanillocalcin
58	AATAGGGGAAA	13	19	4	1	0	0	ESTs, KIA1075 protein
59	GTGCTACTCTT	5	25	2	18	0	0	collagen, type IV, alpha 1
60	CCGGGCCCTCC	6	24	0	0	1	0	peanut (Drosophila)-like 2
61	TTGAATTGTGT	19	10	1	1	0	0	RNA-binding protein gene with multiple splicing
62	CGAGAGTGTA	22	6	0	0	0	0	ESTs
63	CCGTGTTGAC	14	15	38	24	0	0	tyrosine kinase with IgG and EGF homology domains (Tie)

64	CAGATGGAGGC	18	10	1	9	0	ESTs
65	AGGCTCTGCG	8	20	0	0	0	ESTs
66	TCTGCTCTAG	20	8	40	15	0	ESTs
67	GGCTTAGGATG	18	9	10	14	0	ESTs
68	GGTGTGGGG	6	21	0	0	1	ESTs
69	ACAAGTACCA	5	22	4	5	0	P311 protein
70	CTTCTCTTGAG	18	9	1	4	1	basic transcription element binding protein 1
71	GCTAATAATGT	10	17	0	2	0	KIAA1077 protein
72	TGTGCTTTTT	10	15	1	4	0	KIAA0758 protein / protein kinase, cAMP-dependent, catalytic, alpha
73	CATCACGGATC	17	8	0	1	0	interleukin 1 receptor, type I
74	GCAGCAGCAGC	6	18	0	2	0	T-box 2
75	TGACTGTATTA	13	11	0	0	0	ESTs / amine oxidase, copper containing 3 (vascular adhesion protein 1)
76	GAATGCTCTTG	6	18	0	11	0	gap junction protein, alpha 4, 37kD (connexin 37)
77	GTAGTCTCTGGA	18	8	0	5	0	ESTs, clone 23698 mRNA
78	TCCTCTCTCTC	6	17	0	0	0	peridontal ligament fibroblast protein
79	GGCAGTGCGCT	5	18	12	5	0	ESTs, DKFZP686B0621 protein
80	AAATATGTGT	19	4	13	3	0	ESTs
81	GTCTTTTCTTA	11	11	10	2	0	transcription factor 8 (represses interleukin 2 expression)
82	CTCTCCAAACC	14	8	0	0	0	complement component 1 inhibitor (angioedema, hereditary)
83	TTAATGTGTA	4	18	0	0	0	guanylate cyclase 1, soluble, beta 3
84	TCAAGCAATCA	13	9	0	1	0	ESTs
85	GAAGACACTTG	15	7	1	0	0	ESTs
86	GGGTAGGGTGA	6	15	0	0	1	integrin, alpha 7
87	TGGAACAGTGA	10	10	10	5	0	ESTs
88	GAGTGGGTACC	10	9	0	0	0	decidual protein induced by progesterone
89	GTCAGGGGTCC	13	7	0	9	0	halcy (Drosophila)-homolog
90	GTCAGTCACTT	14	8	4	1	0	natriuretic peptide receptor A - guanylate cyclase A
91	AGCAGAGACAA	14	6	1	10	0	ESTs
92	AGCGATGGAGA	9	10	0	0	0	ESTs
93	CGTGGGGTGA	9	10	17	3	0	ESTs

TEM's complete web table

Table 2. SAGE tags elevated in tumor endothelium. The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. †, multiple tags for this gene are due to alternative polyadenylation sites.

no	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	GGGGCTGGCGCA	0	28	0	2	0	ESTs, similarity to thrombospondin
2	GATCTCCGTGT	0	25	0	0	0	ESTs, similarity to rat Rhes ras-related protein
3	CATTCTTATCT	0	23	0	0	0	ESTs
4	CTTCTTTTGG	0	22	6	20	1	regulated in glioma-like 7-1 (Dkk-3) REIC
5	TATTAAGTCTC	0	21	1	3	1	ESTs, similarity to JNK interacting protein-3a
6	CAGGAGACCCC	0	16	2	0	0	MMP-11 (stromelysin 3)
7	GGAATGTCAA	1	31	53	22	1	MMP-2 (gelatinase A, 72KD type IV collagenase)
8	CCTGGTTCAGT	0	15	0	0	0	ESTs
9	TTTTTAAGAAC	0	14	1	4	0	ESTs
10	TTTGGTTTTTC	5	139	0	16	0	collagen, type I, alpha 2, transcript A'
11	ATTTTGTATGA	0	13	4	8	0	nidogen (entactin)
12	ACTTTAGATGG	1	23	0	15	0	collagen, type VI, alpha 3
13	GAGTGAGACCC	3	63	0	0	1	Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	0	ESTs / cystatin S
15	CCACAGGGGAT	2	38	0	2	1	collagen, type III, alpha 1
16	TFAAAGTCCAC	1	19	1	3	1	ESTs
17	ACAGACTGTTA	4	74	0	0	0	ESTs, similarity with sea squirt nidogen
18	CCACTGCAACC	1	18	0	1	0	ESTs, similarity with homeobox protein DLX-3
19	CTATAGGAGAC	1	18	1	1	0	collagen, type I, alpha 2, transcript B'
20	GTCCACAGAA	0	9	0	3	0	ESTs / pregnancy specific beta-1-glycoprotein 1
21	TACCAAGCTCCG	0	9	4	1	1	endo180 lectin
22	GCCCTTTCTCT	1	17	3	1	2	collagen, type I, alpha 1
23	TFAATAGCAC	2	33	0	4	0	ESTs, DKFZP434G162 protein
24	AGACATACTGA	1	16	1	0	0	bone morphogenetic protein 1 (metalloprotease)
25	TCCGCCAGGAG	1	16	0	0	0	slit (Drosophila) homolog 3 (MEGF5)
26	AGCCCAAGTG	0	8	0	0	0	KIAA0672 gene product
27	ACTACCATAC	0	8	0	0	0	
28	TACAAATCGTT	0	8	0	0	0	

see table 2 from paper for G-1, 12-15 Gv

↑

all

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29	TTGGTGAAAA	0	8	0	0	0	ESTs
30	CATTATCCAAA	0	8	0	0	0	integrin, alpha 1
31	AGAAACCACCG	0	8	2	7	0	collagen, type IV, alpha 1
32	ACCAAACCCAC	0	8	0	3	0	
33	TGAAATAAAC	0	8	3	1	1	
34	TTTGGTTTCC	1	15	0	0	0	ESTs
35	GTGGAGACGGA	1	15	1	2	1	ESTs
36	TTTGTGTGTA	1	14	2	0	0	collagen, typeXII, alpha 1
37	TTATGTTTAT	3	39	0	0	1	lunican
38	TGGAATGACC	15	179	0	40	0	ESTs / collagen, type I, alpha 1
39	TGCCACACAGT	1	13	0	2	0	transforming growth factor, beta 3
40	GATGAGGAGAC	3	35	0	18	1	collagen, type I, alpha 2, transcript C'
41	ATCAAAGGTTT	2	23	0	0	0	ESTs, DKFZp564O222 mRNA
42	AGTCACATAGT	1	11	2	0	0	cell division cycle 42 (GTP-binding protein)
43	TTGGTITGGTC	4	45	0	19	0	
44	CCCCACACGGG	2	21	0	0	0	ESTs
45	GGCTTGCCTTT	1	10	0	10	1	
46	ATCCCTCCCG	1	10	1	0	0	peanut-like protein 1

Table 3. Detection of transcripts in various tumor types by RT-PCR and in situ hybridization (ISH). The "+" sign indicates the presence of a robust RT-PCR product or strong positive staining of vessels by in situ hybridization. The "-" sign indicates an undetectable signal by in situ hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number of vessels by in situ hybridization.

	TEM1	TEM3	TEM4	TEM5	TEM7	TEM8	TEM9	vWF	Hevin
RT-PCR	Colon Nor.	-	-	-	-	-	-	+	ND
	Colon Tum.	+	+	+	+	+	+	+	ND
ISH	Colon Nor.	-	-	-	-	-	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+
	Liver Met.	+	+/-	+	+	+	+	+/-	ND
	Lung Tum.	+	ND	+	+	+	+	+	+
	Brain Tum.	+	ND	ND	+	ND	ND	+	+*
	Corpus Lut.	+	+	+	+	-	+	+	+
	Wound	+	ND	+	ND	+/-	+/-	+	+

* hevin was localized to both endothelial cells and malignant cells in brain tissue.

ND: not determined.

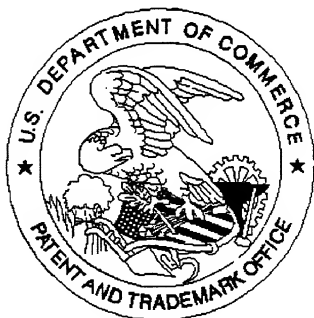
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Table 3. SAGE tags elevated in normal endothelium. The top 48 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	TCTACGGTCT	28	0	0	0	0	mucosal vascular addressin cell adhesion molecule 1
2	CTAGCGTTTT	19	0	4	14	0	serum deprivation response (phosphatidylinositol-binding protein)
3	GTGGCTGACG	18	0	1	0	0	ESTs / Intercellular adhesion molecule 4
4	CTCTTAAAAA	34	1	1	0	0	small inducible cytokine subfamily A (Cys-Cys), member 14
5	TGGGAAGAGG	16	0	3	4	1	ESTs
6	GTTTAAGGAT	16	0	0	0	0	ESTs
7	CTTTGTTTTG	15	0	56	32	1	endothelin 1 / ribosomal protein L27
8	ATTGCCAATC	14	0	0	4	0	TU3A protein
9	TGTTGAAAAA	21	1	1	0	0	selectin E (endothelial adhesion molecule 1)
10	ACAAAAAGGC	21	1	0	6	0	TU3A protein
11	AAGATTGCACAC	21	1	1	1	1	phosphodiesterase 1 - nucleotide pyrophosphatase 2 (autolysin)
12	GTAGAGGAAA	10	0	0	9	0	platelet/endothelial cell adhesion molecule (CD31 antigen)
13	TGTTCAAGG	10	0	0	1	0	ESTs
14	CTCTTCAAAA	19	1	1	0	0	ESTs / small inducible cytokine subfamily A, member 14
15	TATTAATAA	18	1	6	9	1	transforming growth factor, beta receptor II (70-80kD)
16	GAATTCACCA	9	0	1	14	0	ESTs
17	AAGGAGAACT	9	0	0	0	0	small inducible cytokine subfamily A, member 14
18	AATATCTGAC	9	0	2	2	2	active BCR-related gene
19	TCAGTGACCAG	17	1	4	7	2	protein kinase C ϵ
20	GCAAGTGCC	32	2	1	5	0	ESTs
21	TAAATACTTG	8	0	2	0	0	ESTs (2 unigene clusters)
22	GTCATAATT	8	0	1	0	0	ESTs
23	ATAACCTGCA	8	0	0	0	0	signaling lymphocytic activation molecule
24	TGCATCTGTGC	46	3	1	1	0	ESTs / glycogenin 2
25	TAAAGGCACA	15	1	4	3	0	LIM binding domain 2
26	GACCGGGGCT	73	5	11	7	0	claudin 5
27	ACTCGGTGT	14	1	0	8	0	ESTs

	27	2	3	1	0	GTP-binding protein ESTs
28 CTCTGAGCT	13	1	0	0	0	
29 TCGTGCTTTG	13	1	4	2	1	ESTs
30 GAGCAGTGTCT	10	1	0	1	0	ESTs
31 CTCTAAAAA	10	1	0	0	1	phospholipase C, beta 4
32 GAAACCCGGT	10	1	7	15	1	ESTs
33 AACACAGTGC	10	1	7	15	1	ESTs

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